Supplementary Information– FileS1

J.L. Campos and B. Charlesworth 2019 *The effects on neutral variability of recurrent selective sweeps and background selection*

S1. Approximations for the effect of BGS

Here we use Equation 7 of Nordborg *et al.* (1996), modified to include a contribution from gene conversion to the frequency of recombination, plus an additional term arising from deleterious mutations that were in initially in repulsion with a new neutral variant (Santiago and Caballero 1998; Charlesworth 2012b). This was overlooked in the treatment of BGS by Hudson and Kaplan (1995) and Nordborg *et al.* (1996), but can play a significant role with diploidy. With low frequencies of recombination, this term is negligible, but we are dealing cases in which the map length can be considerably larger than one, because of the rescaling of the deterministic parameters in the simulations.

For a given class of deleterious mutations with selection coefficient t, occurring at a net rate U_t over the region in question, the Nordborg *et al.* equation is:

$$E_{t1} \approx \frac{U_t t}{l}\left\{\int_0^{Pl} \frac{\mathrm{d}z}{[t+g(1-t)+c(z)(1-t)]^2} + \int_0^{Ql} \frac{\mathrm{d}z}{[t+g(1-t)+c(z)(1-t)]^2}\right\} \quad \text{(S1a)}$$

where l is the length of the region in basepairs, Pl is the distance from the left-hand end of the region to the location of the neutral site, and $Q = 1 - P$. The other variables are defined before Equation 1 in the main text.

Using the expression for the second BGS term (Charlesworth 2012b), there is an additional contribution of:

$$E_{t2} \approx \frac{U_t t}{l}\left\{\int_0^{Pl} \frac{[t+2g(1-t)+2c(z)(1-t)]^2\,\mathrm{d}z}{[t+g(1-t)+c(z)(1-t)]^2} + \int_0^{Ql} \frac{[t+2g(1-t)+2c(z)(1-t)]^2\,\mathrm{d}z}{[t+g(1-t)+c(z)(1-t)]^2}\right\} \quad \text{(S1b)}$$

Assuming a fixed rate g of gene conversion (see Theoretical Results section of the main text), and transforming to $x = \exp(-2r_c z)$, the indefinite integral corresponding to the integrals inside the braces in Equation S1a can be written as:

$$I_1 = (-2r_c)^{-1} \int \frac{\mathrm{d}x}{x[t+g(1-t)+\frac{1}{2}(1-x)(1-t)]^2} \quad \text{(S2a)}$$

Writing $a = t + g(1 - t) + ½ (1 - t) = ½ (1 + t) + g(1 - t)$ and $b = - ½ (1 - t)$, we have:

$$I_1 = (2r_c)^{-1}\left\{\frac{1}{a^2}\ln\left(\frac{a+bx}{x}\right) - \frac{1}{a(a+bx)}\right\} \qquad \text{(S2b)}$$

Similar calculations can be done for the case of a linear relation between map distance and physical distance, such that $c(z) = r_c z$. In this case, we replace a and b with $a' = t + g(1 - t)$, $b' = 1 - t$, and write $y = r_c z$, giving the equivalent of Equation S2b as:

$$I_1' = (-r_c)^{-1}(a' + b'y)^{-2} \qquad (b' \neq 0) \qquad \text{(S2c)}$$

$$I_1' = r_c y \qquad (b' = 0) \qquad \text{(S2d)}$$

The definite integrals in Equation S1a sum to $I[x(Pl)] + I[x(Ql)] - 2I[x(0)]$, where $x(0) = 1$, $x(Pl)\exp(-2r_cPl)$ and $x(Ql) = \exp(-2r_cQl)$. In order to avoid complicated integrations, we assume that the mean effect of BGS over the whole region can be approximated by the value for $P = Q = ½$, as suggested by Figure 2 of Nordborg *et al.* (1996). Equation S1a then gives:

$$E_{1t} \approx 2U_t t l^{-1}\{I[x(l) - I[x(0)]\} \qquad \text{(S3)}$$

Following Nordborg *et al.* (1996), Equations S2 can be simplified when $M(1 - t) >> t + g(1 - t)$, to give the following expression for E_{1t} for the linear map model (terms in gt have been neglected):

$$E_{1t} \approx 2U_t t(t + g)^{-1} M^{-1} \qquad \text{(S4a)}$$

Using the Taylor series expansion of E_{1t} with respect to t, we obtain the following approximation to the expectation of E_{1t} over the distribution of t for the linear map:

$$\bar{E}_1 \approx 2U_t(g + \bar{t})^{-1}[\bar{t} - gV(t)(g + \bar{t})^{-2}] \qquad \text{(S4b)}$$

where $V(t)$ is the variance of t over the truncated gamma distribution of mutational effects on fitness. For ease of numerical work, $V(t)$ can be further approximated by the variance of

the untruncated gamma distribution. Equation S4b is, however, not necessarily accurate for the rescaled parameters used in the simulations, since the condition on the relation between M and t is likely to be violated (see Table S2).

We now consider the second contribution to the BGS effect. The indefinite integral in Equation S1b can be evaluated in the same way as for Equation S1a. For the Haldane mapping function, the numerator of Equation S1b is a quadratic in x, giving:

$$I_2 = (-2r_c)^{-1} \int \frac{(d^2 + 2dex + e^2x^2)\mathrm{d}x}{x(a+bx)^2} \qquad \text{(S5a)}$$

where $d = 1 + 2g(1 - t)$ and $e = -(1 - t)$.

The first component in the numerator simply contributes d^2E_{1t} to the final expression for the net contribution to the BGS effect, E_{2t}. The second component involves:

$$r_c^{-1}d(1-t)\int \frac{\mathrm{d}x}{(a+bx)^2} = -\frac{d(1-t)}{r_c b(a+bx)} \qquad \text{(S5b)}$$

The third component involves:

$$(-2r_c)^{-1}e^2 \int \frac{x\,\mathrm{d}x}{(a+bx)^2}$$

$$= \frac{e^2}{2r_c b^2}\left\{\frac{a}{(a+bx)} + \ln(a+bx)\right\} \qquad \text{(S5c)}$$

After multiplication by $U_t t$, the corresponding definite integrals between $x = 1$ and $x = \exp(-r_c l)$ can be used to calculate the relevant contributions to E_{2t}, in the same way as for E_{1t}.

The final value for the BGS effect for a given t is $E_t = E_{1t} + E_{2t}$. It is useful to note that l can be written as M/r_c, where M is the map length of the region in question, so that the factor of r_c in Equations S2 and S5 can be cancelled, and M substituted for l in the divisor of Equations S1 and S3.

For the linear map model, d and e in Equations S5 are replaced with $d' = t + 2g(1 - t)$ and $e' = 2(1 - t)$. When $t = 1$ ($b' = 0$), the integral is given by Equation S2d. Otherwise, a contribution of d'^2 is added to the term arising from Equation S2c, as with the Haldane mapping function, and the relations corresponding to Equations S5b and S5c are:

$$\frac{2d'e'}{r_c b'^2}\left\{\ln(a'+b'y)+\frac{a'}{(a'+b'y)}\right\} \qquad (b'\neq 0) \quad \text{(S5d)}$$

$$\frac{e'^2}{r_c b'^3}\left\{a'+b'y-2a'\ln(a'+b'y)-\frac{a'^2}{(a'+b'y)}\right\} \qquad (b'\neq 0) \quad \text{(S5e)}$$

The definite integrals for the linear model are evaluated between $y = 0$ and $y = ½l$; otherwise, the same procedure as for the Haldane mapping function is used.

When linkage is tight, the denominator and numerator in Equation S1b for both mapping functions are approximately equal. This implies that the final contribution in both cases is approximately equal to $2U_t t$, which is equal to the additive genetic variance (V_A) contributed by the whole region (Mukai *et al.* 1972; Santiago and Caballero 1998; Charlesworth 2012a). The expected value of E_{2t} over the distribution of t is thus:

$$\bar{E}_2 \approx 2U_t\bar{t} = V_A \qquad \text{(S6)}$$

For completely free recombination, the contribution is four times this expression (Santiago and Caballero 1998; Charlesworth 2012a). Use of V_A thus provides a conservative approximation.

The results in Table S2 show that the full treatment of the linear model gives quite accurate fits to the simulation results for the lower crossing over rates, but becomes somewhat inaccurate for the two highest values, as might be expected since it overestimates the amount of crossing over when there is no interference.

S2. Variance of the first passage time of a neutral mutation and variance of the time to fixation following the first stochastic phase

Following Kimura and Ohta (1973), the time $T(x)$ that a mutation with initial frequency $1/(2N)$ spends between $1/(2N)$ and a higher frequency x, conditional on not returning to a frequency below $1/(2N)$, is given by the relation:

$$T_f(1/2N) = T(x) + T_f(x) \qquad \text{(S7)}$$

where $T_f(p)$ is the time to fixation of a variant with initial frequency p.

Since $T_f(1/2N)$ and $T_f(x)$ are generated by independent stochastic events, the variance of $T(x)$ is:

$$V\{(T(x)\} = V\{T_f(1/2N)\} - V\{T_f(x)\} \qquad \text{(S8a)}$$

Using Equation 11 of Kimura and Ohta (1973) for the mean time to fixation of a neutral mutation, the mean value of $T(x)$ is approximately $B_1 x$ if x and $1/(2N)$ are both << 1, as in the case of interest here. When $x = (B_2\gamma)^{-1}$, $B_1 x = \lambda\gamma^{-1}$ (with $\lambda = B_1/B_2$). Their Equation 14 gives the mean square of the fixation time for an assumed initial frequency. Using these expressions and neglecting second-order terms, after some tedious algebra we obtain:

$$V\{(T(x)\} \approx \tfrac{1}{3} B_1^2 x^2 \qquad \text{(S8b)}$$

Putting $B_1 x = \lambda\gamma^{-1}$, we have:

$$V\{(T(x)\} \approx \tfrac{1}{3} B_1^2 x^2 \qquad \text{(S9)}$$

This expression gives an approximation for the variance of the time taken up by the first stochastic phase of an adaptive substitution. We can also find an expression for the variance in the duration of the deterministic phase, resulting from variation in the frequency of A_2 at the end of the first stochastic phase (Martin and Lambert 2015). Using the argument leading to Equation 3, this time is given approximately by $4\gamma^{-1}\ln(q_0)$, where q_0 is the initial frequency of A_2 at the end of the first stochastic phase. Since q_0 is exponentially distributed, with mean $(B_2\gamma)^{-1}$ and variance $(B_2\gamma)^{-2}$ (Martin and Lambert 2015), the delta method for approximating the variance of a function of a variable with known variance gives the variance of $\ln(q_0)$ as ≈ 1, and the variance of this component of the fixation time as $16\gamma^{-2}$.

S3. Coalescence of a swept allele during the sweep

The mean coalescent time for a population of varying size can be approximated by replacing N_e by the harmonic mean of the effective population sizes over the period in question (Slatkin and Hudson 1991). We consider a lineage at the time of completion of a sweep, assuming that it traces its ancestry back to the selectively favored allele A_2 at the end of the first stochastic phase, i.e. conditional on no recombination having occurred. The neutral effective population size for this lineage during the second stochastic phase is close to $2B_1$, and the duration of this phase (section S2) is approximately $\lambda\gamma^{-1}$, so that the net contribution to the integral of the reciprocal of the neutral effective population size over the

entire period, measured relative to $2N_e$, is $\lambda(B_1\gamma)^{-1}$. The second contribution arises from the deterministic phase. If the frequency of A_2 at time T (in units of $2N_e$ generations) is $q(T)$, the corresponding relative effective population size for the lineage under consideration is $B_1q(T)$. The integral of the reciprocal of this quantity over the deterministic phase is given by:

$$\int_{T_0}^{T_1} \frac{\mathrm{d}T}{B_1 q(T)} = 2\gamma^{-1} \int_{(B_2\gamma)^{-1}}^{1-(B_2\gamma)^{-1}} \frac{\mathrm{d}q}{B_1 p q^2}$$
$$\approx 2(B_1\gamma)^{-1}\{2\ln(B_2\gamma) + B_2\gamma - [1-(B_2\gamma)^{-1}]^{-1}\} \qquad \text{(S10)}$$

The mean coalescent time arising from these two contributions is the main contribution to the overall relative mean coalescent time for a swept lineage, T_{cs}, since coalescence happens very rapidly during the initial stochastic phase. T_{cs} is thus given by dividing the net time for the sweep (Equation 3 of the main text), by the sum of $\lambda(B_1\gamma)^{-1}$ and Equation S9:

$$T_{cs} \approx \frac{B_1[2\ln(B_2\gamma) + \lambda]}{2\ln(B_2\gamma) + \lambda^{-1} + B_2\gamma - [1-(B_2\gamma)^{-1}]^{-1}} \qquad \text{(S11)}$$

If $B_2\gamma >> 1$, T_{cs} is approximately equal to $1/[1 + \frac{1}{2} B_2\gamma/\ln(B_2\gamma)]$. This is not necessarily totally negligible; for example, if $B_2\gamma = 100$, $T_{cs} \approx 0.08$, i.e. approximately 8% of the neutral variability in the absence of selection is expected to be recovered by the end of the sweep.

S4. Recombination back onto the A_2 background during a sweep

A process that works in the opposite direction to the effect of recovery of variability is recombination of a swept lineage that has recombined onto an A_1 background back onto an A_2 background (Figure 2). This effect can be analysed as follows, by examining the trajectory of the probability $P(T)$ that a lineage associated with A_2 was present on an A_2 background at a given time T in the past, with $P(T_s)$ being the net probability that the ancestor of the lineage was associated with A_2.

Let $p(T)$ be the frequency at time T of the wild-type allele at the selected locus, and $q(T) = 1 - p(T)$. If recombination occurs at rate $\rho = 2N_e r$ on the coalescent timescale, and all evolutionary changes are slow, P obeys the following differential equation:

$$\begin{aligned}\frac{\mathrm{d}P(T)}{\mathrm{d}T} &= -\rho p(t)P(T) + \rho q(T)[1 - P(T)] \\ &= -\rho P(T) + \rho q(T) \qquad \text{(S12)}\end{aligned}$$

The boundary condition is $P(0) = 1$, yielding the solution:

$$P(T) = \exp(-\rho T)[1 + \rho \int_0^T \exp(\rho\tau) q(\tau)\,\mathrm{d}\tau] \qquad \text{(S13)}$$

The integral can be evaluated by substituting $\mathrm{d}p(\tau)$ for $\mathrm{d}\tau$; using the backwards-in- time selection equation, $\mathrm{d}p/\mathrm{d}T \approx 0.5\gamma pq$, we obtain:

$$\int_0^T \exp(\rho\tau) q(\tau)\,\mathrm{d}\tau = 2(\gamma)^{-1} \int_{p(0)}^{p(T)} \exp[\rho\,\tau(p)] p^{-1}\mathrm{d}p \qquad \text{(S14)}$$

where

$$\tau(p) \approx 2(\gamma)^{-1} \ln(B_2 \gamma p q^{-1}) \qquad \text{(S15)}$$

This assumes that the initial value of q for a successful sweep is $(B_2\gamma)^{-1}$, on the grounds that the contribution from the first stochastic phase is negligible, given the low frequency of A_2 over this period. The exponential term can thus be written as $(B_2\gamma)^a p^a q^{-a}$, where $a = 2\rho\gamma^{-1}$.

We are primarily interested in $P(T_s)$, for which the integral takes the value:

$$\int_0^{T_s} \exp(\rho\tau) q(\tau)\,\mathrm{d}\tau = 2(\gamma)^{-1} (B_2\gamma)^a \int_{p(0)}^{p(T_s)} p^{a-1} q^{-a}\,\mathrm{d}p \qquad \text{(S16)}$$

We can set $p(T_s) = 1$ and $p(0) = (B_2\gamma)^{-1}$ to a sufficient level of accuracy, so that the definite integral in equation (S15) is equivalent to:

$$\begin{aligned}&\int_0^1 p^{a-1} q^{-a}\,\mathrm{d}p - \int_0^{(B_2\gamma)^{-1}} p^{a-1} q^{-1}\,\mathrm{d}p \\ &\approx \mathrm{B}(a, 1-a) - a^{-1}(B_2\gamma)^{-a} \qquad \text{(S17)}\end{aligned}$$

where B(a, 1 – a) is the beta function with parameters a and 1 – a.

From the known properties of the beta function, B(a, 1 – a) = π /sin(πa). For a << 1, π /sin(πa) ≈ $a^{-1}[1 + (\pi a)^2/6]$, so that:

$$\int_0^{(B_2\gamma)^{-1}} p^{a-1}q^{-a}\mathrm{d}p \approx a^{-1}[1+\tfrac{1}{6}(\pi a)^2 - (B_2\gamma)^{-a}] \qquad \text{(S18)}$$

This yields:

$$P(T_s) \approx \exp(-\tfrac{1}{2}\rho T_s)[1+\tfrac{2}{3}(\pi\rho\gamma^{-1})^2] \qquad \text{(S19)}$$

The probability that two alleles have not recombined by the end of the sweep is thus:

$$P_{cs} \approx \exp(-\rho T_s)[1+\tfrac{2}{3}(\pi\rho\gamma^{-1})^2]^2 \qquad \text{(S20)}$$

This replaces the expression exp(–ρT_s) in the standard formula.

S5. Correcting for the effect of sweep duration

Here we derive expressions for the integral $I(\omega, B_1)$ in Equation 11. For $B_1\omega > 1$, I can be evaluated by using the fact that:

$$\omega\int_0^\infty x^i \exp(-\omega x)\,\mathrm{d}x = i!\,\omega^{-i} \qquad \text{(S21)}$$

Expanding exp($-B_1^{-1}T$) in Equation 11 as its MacClaurin series in $B_1^{-1}T$, and substituting into the double integral, we have:

$$\begin{aligned}\omega B_1 I(\omega, B_1) &= \omega B_1 \int_0^\infty \sum_{i=0}^\infty \exp(-\omega T)\left[\frac{B_1^{-(i+1)}(-1)^i T^i}{(i+1)!}\right]\mathrm{d}T \\ &= [1+\sum_{i=1}^\infty (-1)^i (i+1)^{-1}(B_1\omega)^{-i}] = \omega B_1 \ln[1+(B_1\omega)^{-1}] \qquad \text{(S22)}\end{aligned}$$

As $B_1\omega$ approaches 1, this expression implies that $I(\omega,B_1)$ tends to $\ln(2) \approx 0.6931$, although the series is not formally convergent at this point, but behaves as an asymptotic expansion. For $B_1\omega < 1$, $I(\omega, B_1)$ can be expanded as a Taylor series in ω around $\omega = B_1^{-1}$, using the fact that its ith derivative with respect to $B_1\omega$ is equal to $(-1)^i(i-1)![(B_1\omega)^{-i} - (1+B_1\omega)^{-i}]$. This gives:

$$I(\omega,B_1) = \ln(2) + \sum_{i=1}^{\infty}(-1)^i i^{-1}(1-2^{-i})(B_1\omega-1)^i \qquad \text{(S23)}$$

Numerical evaluation shows that, for small $B_1\omega$, the series converges slowly to a finite limit. For $\omega = 0.001$, the limit is approximately 6.908. With $\omega \geq 0.1$, the series effectively converges to a limit ≤ 2.398 after $i \leq 100$.

S6. Sampling during a sweep

Let the rates of coalescent events due to NS and UTR mutations be S_a^{-1} and S_u^{-1}, respectively; these are given by the corresponding terms in Equations 5, with $S^{-1} = S_a^{-1} + S_u^{-1}$. Let the expected durations of NS and UTR adaptive substitutions be T_a and T_u, respectively; these are obtained by substituting γ_a and γ_u into Equation 3. Using Equation S11, the corresponding expected coalescence times for samples taken at the end of successful NS and UTR sweeps are T_{acs} and T_{ucs}. The probability that a random sample is not included in a sweep is $P_{ns} = [S_a^{-1}\exp(-S^{-1}T_a) + S_u^{-1}\exp(-S^{-1}T_u)]/S^{-1}$; the value of π/θ given by Equations 12 is to be multiplied by this quantity to obtain the net contribution from this type of event. Upper bounds to the expected coalescent times for a sample taken during an NS or UTR sweep are given by T_{acs} and T_{ucs} respectively. The net coalescent time contribution from samples taken within sweeps is obtained by weighting these times by the probabilities of sampling each type of sweep, i.e. by $(S_a^{-1}T_{acs}[1-\exp(-S^{-1}T_a)] + S_u^{-1}T_{ucs}[1-\exp(-S^{-1}T_a)])/S^{-1}$. The sum of this term and the previous one provides an estimate of the net relative diversity.

S7. Continuum approximation for effects of recurrent selective sweeps

For NS sites, consider a focal synonymous site located at a site representing a proportion P of the total length l of the coding sequence. For $lP \leq d_g$, the expected contribution to S^{-1} in Equations 5 of the main text, caused by sweep events at NS sites to the left of the focal site, is equal to:

$$S_{1P}^{-1} \approx \upsilon_a \int_0^{lP} \exp[-4\xi_a(r_c + r_g)z]\mathrm{d}z$$
$$= \frac{\upsilon_a}{4\xi_a(r_c + r_g)}\{1 - \exp[-4\xi_a(r_c + r_g)lP]\} \qquad \text{(S24a)}$$

where $\xi_a = \lambda\,[\ln(B_2\gamma_a) + 0.5]\,/s_a$.

Writing $Q = 1 - P$, a similar expression holds for the effects of sweeps at NS sites to the right of a focal site when $Ql \le d_g$:

$$S_{1Q}^{-1} \approx \nu_a \int_0^{lQ} \exp[-4\xi_a(r_c + r_g)z]\mathrm{d}z$$
$$= \frac{\nu_a}{4\xi_a(r_c + r_g)}\{1 - \exp[-4\xi_a(r_c + r_g)lQ]\} \qquad \text{(S24b)}$$

The mean value over all synonymous sites for these two cases can be found by integrating the sum of these two expressions with respect to P and Q, respectively, from 0 to their maximum permissible value, $d_g\,/l$. By symmetry, no distinction need be made between P and Q, so we have:

$$S_1^{-1} \approx \frac{2\nu_a}{4\xi_a(r_c + r_g)} \int_0^{d_g/l} \{1 - \exp[-4\xi_a(r_c + r_g)l\,x]\}\,\mathrm{d}x$$
$$= \frac{\nu_a}{2\xi_a(r_c + r_g)}\left(\frac{d_g}{l} - \frac{1}{4\xi_a(r_c + r_g)l}\{1 - \exp[-4\xi_a(r_c + r_g)d_g]\}\right) \qquad \text{(S25)}$$

For $l\,P > d_g$, the expected contribution to S^{-1} from single sweeps at NS sites to the left of the focal site is equal to:

$$S_{2P}^{-1} \approx \nu_a \int_0^{d_g} \exp[-4\xi_a(r_c + r_g)z]\mathrm{d}z + \exp(-4\xi_a g)\int_{d_g}^{lP} \exp[-4\xi_a r_c z]\mathrm{d}z$$
$$= \frac{\nu_a}{4\xi_a(r_c + r_g)}\{1 - \exp[-4\xi_a(r_c + r_g)d_g]\}$$
$$+ \frac{\nu_a \exp(-4\xi_a g)}{4\xi_a r_c}[\exp(-4\xi_a r_c d_g) - \exp(-4\xi_a r_c lP)] \qquad \text{(S26)}$$

As before, a similar expression can be found for NS sites to the right of the focal site, by substituting Q for P.

The mean value for synonymous sites of this type can be found by integrating with respect to P, from $P = d_g/l$ to $P = 1$, and from $Q = d_g/l$ to $Q = 1$, yielding:

$$\begin{aligned} S_2^{-1} = & \frac{(1-d_g/l)\nu_a}{2\xi_a(r_c+r_g)}\{1-\exp[-4\xi_a(r_c+r_g)d_g]\} \\ & + \frac{\exp(-4\xi_a g)\nu_a}{2\xi_a r_c}\{(1-d_g/l)\exp(-4\xi_a r_c d_g) \\ & - \frac{\nu_a}{2\xi_a r_c l}[\exp(-4\xi_a r_c d_g)-\exp(-4\xi_a r_c l)]\} \end{aligned} \qquad \text{(S27a)}$$

If there is no gene conversion, $d_g = g = 0$, and Equation S27a reduces to:

$$S_2^{-1} = \frac{\nu_a}{2\xi_a r_c}\left\{1-\frac{1}{4\xi_a r_c l}[1-\exp(-4\xi_a r_c l)]\right\} \qquad \text{(S27b)}$$

The effects of sweeps in 5′UTRs, whose length is denoted by l_0, can be found as follows. Subscripts u are used to denoted the parameters corresponding to ξ_a etc. in the treatment of NS sites. Consider a focal synonymous site at location lP. Its distance from a 5′UTR site that is located at a distance y from the beginning of the coding sequence is $z = lP + y$. Note that, for the gene conversion parameters assumed in the simulations, we have $l_0 < d_g$, but this is not necessarily the case – the case with no gene conversion is equivalent to setting $d_g = 0$.

First, assume $l_0 < d_g$. With $z < d_g$, so that gene conversion occurs approximately at rate $(r_c + g_c)z$, y runs from 0 to l_0 and lP runs from 0 to $d_g - y$. The expected contribution of single sweeps in the UTR for a synonymous site is given by:

$$S_3^{-1} \approx \nu_u \int_0^{l_0} \int_0^{(d_g-y)/l} \exp[-4\xi_u(r_c+r_g)(y+lP)]\,\mathrm{d}P\,\mathrm{d}y$$
$$= \frac{\nu_u}{4\xi_u(r_c+r_g)l} \int_0^{l_0} \exp[-4\xi_u(r_c+r_g)y]\{1-\exp[-4\xi_u(r_c+r_g)(d_g-y)]\}\,\mathrm{d}y$$
$$= \frac{\nu_u}{4\xi_u(r_c+r_g)l} \left\{ \frac{1}{4\xi_u(r_c+r_g)} (1-\exp[-4\xi_u(r_c+r_g)l_0]) - l_0 \exp[-4\xi_u(r_c+r_g)d_g] \right\} \qquad \text{(S28)}$$

With $z \geq d_g$, so that gene conversion occurs at rate g, y runs from 0 to l_0 and lP runs from $d_g - y$ to l; the expected contribution of UTR sweeps is then:

$$S_4^{-1} \approx \nu_u \int_0^{l_0} \int_{(d_g-y)/l}^{1} \exp\{-4\xi_u[r_c(y+lP)+g]\}\,\mathrm{d}P\,\mathrm{d}y$$
$$= \frac{\nu_u \exp(-4\xi_u g)}{4\xi_u r_c l} \int_0^{l_0} \exp(-4\xi_u r_c y)\{\exp[-4\xi_u r_c(d_g-y)] - \exp(-4\xi_u r_c l)\}\,\mathrm{d}y$$
$$= \frac{\nu_u \exp(-4\xi_u g)}{4\xi_u r_c l} \left\{ l_0 \exp(-4\xi_u r_c d_g) - \frac{\exp(-4\xi_u r_c l)}{4\xi_u r_c} [1-\exp(-4\xi_u r_c l_0)] \right\} \qquad \text{(S29)}$$

Second, consider the case $d_g \leq l_0$. With $z < d_g$, y runs from 0 to d_g and lP runs from 0 to $d_g - y$. This implies that l_0 can be replaced with d_g in the last line of Equation S28:

$$S_5^{-1} \approx \nu_u \int_0^{d_g} \int_0^{(d_g-y)/l} \exp[-4\xi_u(r_c+r_g)(y+lP)]\,\mathrm{d}P\,\mathrm{d}y$$
$$= \frac{\nu_u}{4\xi_u(r_c+r_g)l} \left\{ \frac{1}{4\xi_u(r_c+r_g)} (1-\exp[-4\xi_u(r_c+r_g)d_g]) - d_g \exp[-4\xi_u(r_c+r_g)d_g] \right\} \qquad \text{(S30)}$$

When $z \geq d_g$, two cases need to be considered. If $y \leq d_g$, lP runs from $d_g - y$ to l, giving the integral:

$$S_6^{-1} \approx \nu_u \int_0^{d_g} \int_{(d_g-y)/l}^{1} \exp\{-4\xi_u[r_c(y+lP)+g]\}\,\mathrm{d}P\,\mathrm{d}y$$
$$= \frac{\nu_u \exp(-4\xi_u g)}{4\xi_u r_c l}\left\{d_g \exp(-4\xi_u r_c d_g) - \frac{\exp(-4\xi_u r_c l)}{4\xi_u r_c}[1-\exp(-4\xi_u r_c d_g)]\right\} \quad \text{(S31)}$$

If $y > d_g$, lP runs from 0 to l, giving the integral:

$$S_7^{-1} \approx \nu_u \int_{d_g}^{l_0} \int_0^1 \exp\{-4\xi_u[r_c(y+lP)+g]\}\,\mathrm{d}P\,\mathrm{d}y$$
$$= \frac{\nu_u \exp(-4\xi_u g)[1-\exp(-4\xi_u r_c l)]}{(4\xi_u r_c)^2 l}[\exp(-4\xi_u r_c d_g) - \exp(-4\xi_u r_c l_0)] \quad \text{(S32)}$$

The final result is given by the sum of these two expressions.

If there is no gene conversion (so that $d_g = 0$), only Equation S32 is relevant, which reduces to:

$$S_7^{-1} \approx \nu_u \int_0^{l_0} \int_0^1 \exp\{-4\xi_u[r_c(y+lP)+g]\}\,\mathrm{d}P\,\mathrm{d}y$$
$$= \frac{\nu_u[1-\exp(-4\xi_u r_c l)][1-\exp(-4\xi_u r_c l_0)]}{(4\xi_u r_c)^2 l} \quad \text{(S33)}$$

Similar results hold for 3′UTRs, whose length is denoted by l_1; l_0 is simply replaced with l_1 in the above expressions.

S8 Inferring the parameters of interference among selective sweeps

For a given parameter set and number of genes, we can treat each gene in a given simulation run as an independent replicate, and estimate the variance from the 95% confidence intervals for the total numbers of NS or UTR adaptive substitutions per chromosome for a given number of genes (File S3) (because the Central Limit Theorem implies that these are normally distributed, the C.I. for a given parameter set is equal to $1.96\sigma/\sqrt{n}$, where σ is the standard deviation and n is the number of replicate simulations). This assumes that there is little interference among substitutions in different genes, which is justified by the lack of effect of the number of genes on the numbers of substitutions when crossing over is present (Tables 3 and S4).

The ratio of the mean to the variance (R) is distributed approximately as χ^2, with the number of degrees of freedom (d.f.) equal to the number of replicates minus one. χ^2 and

d.f. values for different parameter sets can be summed to provide an overall test of significance, and the ratio of χ^2 to the d.f. provides an estimate of R. The results are shown in Table S5 below. There is little evidence for an effect of the selection model or the crossing over rate on the estimates of R, consistent with the lack of a strong effect of the crossing over rate on the numbers of adaptive substitutions. For all parameter sets, the total χ^2 is 4639, with 5083 d.f., and Fisher's normal deviate transformation is – 4.50 ($P < 10^{-4)}$. The overall R estimate is 0.91, with an approximate standard error of 0.02.

There is no simple formula for relating R to the intensity of interference, in the sense of the proportion of adaptive substitutions that are removed by interference among sweeps within the same gene. Such interference can only occur when a second substitution is initiated while a given substitution is spreading through the population (Barton 1995; Kim and Stephan 2003). The effects of interference on dispersion were simulated by assigning an adaptive substitution rate of ω per gene per unit coalescent time, and drawing a set of successive exponential random deviates with ω as parameter over the chosen period of observation ($8N$ generations in the case of our simulations), which represent the times between substitutions. If a given substitution is followed by a second one within the time T_s for completion for the first one (Equation 3), the second one is removed with an assigned probability p_i. By replicating this process many times, both R and the proportion of substitutions lost to interference can be estimated. A computer program for this simulation is available (File S4). Using a value of 0.1 for T_s, which is approximately the value for autosomal NS and UTR favorable mutations, together with ω values corresponding to the autosomal loci parameters, $R = 0.91$ corresponds to a net proportion of lost substitutions of approximately 0.055.

S9. BGS effects for regions with selection on noncoding sites

To extend the model of BGS here, which includes the effect of gene conversion, we modified the approach of Charlesworth (2012b), which models a length of chromosome subject to deleterious mutation, with a linear genetic map in the absence of gene conversion, assuming a relative rate of crossing of 1 in the terminology used here. His Table 2 shows that the ratio of the diploid deleterious mutation rate to the effective map length provides a good approximation to the BGS parameter B_1 obtained from more realistic models. In order to include the effects of gene conversion, we used the BGS

formulae given in the first section of the Appendix. Since we are interested in predicting the effects of BGS for parameters that are realistic for a natural population, we used the versions of these formulae that assume a linear genetic map, and ignored contributions from deleterious mutations that are initially in repulsion with a focal neutral variant, i.e. Equations S2c, S2d, S3 and S4a. (The reasons for doing this are explained in the final part of the Discussion.) For this purpose, we used the selection, mutation and recombination parameters that apply to a population that is 532 times as large as the simulated population. Numerical integration of Equation (S3) over the relevant gamma distribution of selection coefficients then allowed us to calculate the ratio of the value of $E = -\ln(B_1)$ with gene conversion at a rate of 2×10^{-8} per base pair to its value without gene conversion for 2000 genes, which gives results close to the asymptote with respect to gene number. For autosomal NS sites, this ratio is 0.816, and for the more weakly selected UTR sites, it is 0.613; these are nearly independent of the rate of crossing over.

We assume that these ratios also apply to the strongly selected and weakly selected sites modeled by Charlesworth (2012b). It is then a simple matter to extract the E values for strongly selected and weakly selected sites for the standard rate of crossing over from the Model 1 results for autosomes in his Table 2, and to modify them by multiplication by a factor of 0.816 and 0.613, respectively. The sum of the resulting products, 0.485, is equal to E for the standard rate of crossing over; the E value for a rate that is a factor of C times the standard rate is given by dividing the standard value by C. The corresponding values of B_1 are then given as $\exp(-E)$.

The same procedure can be applied to the X chromosome, yielding factors of 0.872 and 0.716 for strongly and weakly selected sites, respectively. The resulting E value is 0.4 for the standard rate of crossing over (adjusted so that the effective rate of crossing over is the same for the X and the autosomes).

S10. Diversity patterns on the X chromosome

The procedure used for including effects of BGS on noncoding sequences on autosomes yields X chromosome values of B_1 values of 0.383, 0.619, 0.726, 0.787 and 0.825 for

relative effective rates of crossing over of 0.5, 1, 1.5, 2 and 2.5, respectively, which are very close to the autosomal values. With selective sweeps, these estimates of B_1 yield K values of 2.04 and 1.99 for the smaller and large selection coefficients for favorable X-linked mutations, respectively, compared with an observed value of 1.78 from Figure S2 of Campos et al. (2014).

A possible reason for this is that differences in gene density associated with different crossover rates have been ignored. As noted by Campos *et al.* (2014), the gene density on the X chromosome in regions with low but not zero rates of crossing over is substantially lower than on the autosomes. If the BGS model for the X chromosome is modified to reduce the value of E for the low crossover region by one-quarter, yielding B_1 = 0.487 instead of 0.383, the predicted values of π_S/θ for relative crossover rates of 0.5 and 2 with the weaker selection for favorable X-linked mutations become 0.431 and 0.712, respectively, giving X/A diversity ratios of 0.93 and 0.75 for the two crossover rates after (adjusting the X values by multiplying by 0.75), while the observed values are 1 and 0.74; the value of K for the X is now 1.65, somewhat smaller than the observed value. With the stronger selection case, the respective X/A diversity ratios are 0.92 and 0.69, and K = 1.54.

S11. Rates of substitution of favorable mutations in relation to the rate of crossing over

We used the principle that the expected relative values of ω_a, the rate of adaptive NS substitiutions relative to neutral rates, for different rates of recombination should approximately reflect the corresponding relative values of B_2, given the evidence that there is little interference among positively selected mutations. For autosomes, the B_1 values used here in place of B_2 predict a ratio of 2.08 for crossing over rates of 2 and 0.5, compared with the observed value of approximately 3 from Figure 2 of Charlesworth and Campos (2014). However, Castellano *et al.* (2016) suggested that the smoothing procedure used by them to estimate rates of crossing over for each bin might produce biased results, and instead conducted analyses of the relation between the rate of autosomal NS adaptive evolution and unsmoothed rates of crossing over obtained from Comeron *et al.* (2012). For the Rwandan sample used here, with the same number of bins of rates of crossing over (but including non-crossover regions), their non-linear regression equation (line 5 of their Table 1) yields a ratio of 1.95 for the estimated rates of autosomal adaptive evolution for relative effective rates of crossing over 2 and 0.5, which is much closer to the above prediction. For the X chromosome, the predicted ratio for relative crossover rates of 2 and 1 is 1.27 (the

observed value for 0.5 is not available, due to the binning procedure used), and the observed value from Figure 3 of Charlesworth and Campos (2014) is 1.22.

Literature Cited

Barton, N. H., 1995 Linkage and the limits to natural selection. Genetics 65: 821-841.

Castellano, D., M. Coronado-Zamora, J. L. Campos, A. Barbadilla and A. Eyre-Walker, 2016 Adaptive evolution is substantially impeded by Hill–Robertson interference in *Drosophila*. Mol. Biol. Evol. 33: 442-445.

Charlesworth, B., 2012a The effects of deleterious mutations on evolution at linked sites. Genetics 190: 1-18.

Charlesworth, B., 2012b The role of background selection in shaping patterns of molecular evolution and variation: evidence from the Drosophila *X* chromosome. Genetics 191: 233-246.

Charlesworth, B., and J. L. Campos, 2014 The relations between recombination rate and patterns of molecular evolution and variation in *Drosophila*. Ann. Rev. Genet. 48: 383-403.

Hudson, R. R., and N. L. Kaplan, 1995 Deleterious background selection with recombination. Genetics 141: 1605-1617.

Kim, Y., and W. Stephan, 2003 Selective sweeps in the presence of interference among selected loci. Genetics 164: 389-398.

Kimura, M., and T. Ohta, 1973 The age of a neutral mutation in a finite population. Genetics 75: 199-212.

Martin, G., and A. Lambert, 2015 A simple, semi-deterministic approximation to the distribution of selective sweeps in large populations. Theor. Pop. Biol. 101: 40-46.

Mukai, T., S. I. Chigusa, L. E. Mettler and J. F. Crow, 1972 Mutation rate and dominance of genes affecting viability in *Drosophila melanogaster*. Genetics 72: 335-355.

Nordborg, M., B. Charlesworth and D. Charlesworth, 1996 The effect of recombination on background selection. Genet. Res. 67: 159-174.

Santiago, E., and A. Caballero, 1998 Effective size and polymorphism of linked neutral loci in populations under selection. Genetics 149: 2105-2117.

Slatkin, M., and R. R. Hudson, 1991 Pairwise comparisons of mitochondrial DNA sequences in stable and exponentially growing populations. Genetics 143: 579-587.

Table S1 BGS predictions and simulation results for X chromosomal values of $B_1 = \pi/\theta$

Autosomes

Xover Rate	0.5	1.0	1.5	2.0	2.5
No g.c					
20 genes	0.687, 0.723 (0.702, 0.745)	0.798, 0.838 (0.823, 0.852)	0.845, 0.861 (0.843, 0.879)	0.871, 0.868 (0.849, 0.887)	0.888, 0.913 (0.894, 0.933)
70 genes	0.593, 0.634 (0.623, 0.645)	0.716, 0.737 (0.721,0.750)	0.767, 0.790 (0.770, 0.799)	0.794, 0.818 (0.810, 0.827)	0.812, 0.830 (0.824, 0.838)
140 genes	0.514, 0.543 (0.534, 0.550)	0.632, 0.655 (0.648, 0.663)	0.679, 0.701 (0.694, 0.709)	0.704, 0.723 (0.717, 0.729)	0.719, 0.731 (0.724, 0.739)
210 genes	0.452, 0.489 (0.481, 0.491)	0.559, 0.582 (0.574, 0.590)	0.601, 0.620 (0.618, 0.624)	0.623, 0.642 (0.638, 0.646)	0.637, 0.654 (0.650, 0.658)
G.c.					
20 genes	0.753, 0.796 (0.775, 0.819)	0.836, 0.883 (0.862, 0.903)	0.872, 0.905 (0.889, 0.920)	0.892, 0.907 (0.887, 0.929)	0.905, 0.924 (0.905, 0.942)
70 genes	0.650, 0.686 (0.677, 0.693)	0.750, 0.782 (0.767, 0.799)	0.791, 0.816 (0.797,0.834)	0.813, 0.820 (0.813,0.827)	0.827, 0.838 (0.830,0.848)
140 genes	0.563, 0.594 (0.588, 0.601)	0.662, 0.687 (0.676, 0.696)	0.700, 0.719 (0.707,0.728)	0.720, 0.725 (0.720,0.731)	0.733, 0.736 (0.729,0.744)
210 genes	0.496, 0.525 (0.519,0.531)	0.586, 0.605 (0.598,0.613)	0.620, 0.640 (0.635,0.645)	0.638, 0.639 (0.635,0.640)	0.649, 0.657 (0.652,0.661)

X chromosome

Xover Rate	0.5	1.0	1.5	2.0	2.5
No g.c					
20 genes	0.755, 0.779 (0.757, 0.801)	0.845, 0.880 (0.857, 0.904)	0.881, 0.901 (0.879, 0.922)	0.902, 0.937 (0.923, 0.953)	0.915, 0.928 (0.907, 0.950)
70 genes	0.675, 0.700 (0.693, 0.708)	0.779, 0.807 (0.793,0.823)	0.820, 0.839 (0.830, 0.848)	0.841, 0.860 (0.846, 0.872)	0.856, 0.878 (0.858, 0.884)
140 genes	0.607, 0.627 (0.620, 0.635)	0.709, 0.715 (0.707, 0.724)	0.748, 0.764 (0.759, 0.770)	0.768, 0.788 (0.781, 0.795)	0.781, 0.800 (0.789, 0.810)
210 genes	0.551, 0.571 (0.564, 0.578)	0.647, 0.664 (0.658, 0.670)	0.683, 0.694 (0.689, 0.699)	0.701, 0.719 (0.713, 0.724)	0.713, 0.726 (0.721, 0.733)
G.c.					
20 genes	0.809, 0.840 (0.827, 0.855)	0.875, 0.902 (0.882, 0.922)	0.902, 0.916 (0.898, 0.933)	0.918, 0.941 (0.919, 0.964)	0.928, 0.953 (0.932, 0.974)
70 genes	0.724, 0.756 (0.745, 0.770)	0.806, 0.830 (0.821, 0.841)	0.839, 0.850 (0.838,0.861)	0.856, 0.884 (0.875,0.893)	0.867, 0.878 (0.867,0.889)
140 genes	0.650, 0.682 (0.676, 0.689)	0.734, 0.785 (0.776, 0.793)	0.765, 0.782 (0.776,0.789)	0.782, 0.802 (0.793,0.810)	0.792, 0.805 (0.794,0.816)
210 genes	0.591, 0.623 (0.618, 0.629)	0.670, 0.714 (0.708,0.719)	0.699, 0.720 (0.715, 0.726)	0.714, 0.747 (0.740,0.753)	0.723, 0.739 (0.729,0.751)

The left-hand upper entries in the cells show the predicted values of B_1, the ratio of the mean synonymous site diversity with BGS (but no sweeps) to its value in the absence of BGS (using Equations S1, S2a, S2b, S3, and S5), and integrating over the truncated gamma distribution. The right-hand entries are the corresponding observed mean values.

The lower entries are the lower and upper 2.5 percentiles of the observed values of B_1, obtained from the means of the synonymous site diversities over the entire region for each replicate simulation.

The rows labelled ‘Xover rate’ refer to the results for rates of crossing over with ratios of 0.5, 1, 1.5, etc. with respect to the standard rate of 5.32×10^{-6} used in the simulations.

Cases with no gene conversion are denoted by ‘No g.c.’ and cases with the standard gene conversion parameters by ‘G.c.’

Table S2 BGS predictions with a linear map, and simulation results with the Haldane mapping function. Autosomal values of $B_1 = \pi/\theta$ are shown.

Xover Rate	0.5	1.0	1.5	2.0	2.5
No g.c					
20 genes	0.684, 0.584 0.723	0.802, 0.758 0.838	0.851, 0.828 0.861	0.878, 0.864 0.861	0.898, 0.887 0.913
70 genes	0.609, 0.567 0.643	0.740, 0.732 0.737	0.794, 0.798 0.790	0.823, 0.833 0.818	0.841, 0.855 0.830
140 genes	0.549, 0.538 0.543	0.677, 0.695 0.655	0.727, 0.756 0.701	0.754, 0.789 0.723	0.777, 0.810 0.731
210 genes	0.501, 0.510 0.489	0.621, 0.658 0.582	0.666, 0.717 0.620	0.690, 0.748 0.642	0.704, 0.767 0.654
G.c.					
20 genes	0.763, 0.656 0.796	0.847, 0.804 0.883	0.883, 0.836 0.905	0.903, 0.890 0.907	0.916, 0.908 0.924
70 genes	0.679, 0.636 0.686	0.782, 0.756 0.782	0.823, 0.829 0.816	0.845, 0.857 0.820	0.859, 0.875 0.838
140 genes	0.612, 0.603 0.594	0.715, 0.736 0.687	0.754, 0.786 0.719	0.775, 0.812 0.725	0.787, 0.829 0.736
210 genes	0.558,0.571 0.5250.525	0.655, 0.697 0.605	0.691, 0.745 0.640	0.709, 0.770 0.639	0.719, 0.785 0.657

The first entries in the upper portions of each cell are the values of B_1 obtained from the theoretical predictions for E from the integrals in Equation S2c, S2d, S4a, S5d and S5e, integrated over the truncated gamma distribution.

The second entries are the values of B_1 from the expectation of E given by Equation S4b using the variance from the full gamma distribution, plus the additive variance term in Equation S6. The entries in the lower portions are the mean values from the simulations.

The rows labelled 'Xover rate' refer to the results for rates of crossing over with ratios of 0.5, 1, 1.5, etc. with respect to the standard rate of 5.32×10^{-6} used in the simulations.

The sections labelled 'No g.c.' and 'G.c.' refer to cases with no gene conversion and gene conversion with the standard parameters, respectively.

Table S3 The effect of selective sweeps on the mean number of segregating nonsynymous and UTR site mutations (autosomal 70 gene model)

Xover Rate	**0**	**0.5**	**1.0**	**1.5**	**2.0**	**2.5**
No g.c.	0.987 0.934	0.740 0.715	0.833 0.811	0.844 0.794	0.881 0.789	0.867 0.757
G.c.	1.028 1.110	0.861 0.791	0.833 0.781	0.914 0.773	0.898 0.839	0.921 0.839

The upper entries in each cell are the ratios of the mean numbers of segregating deleterious NS mutations per individual in the presence of SSWs to the mean numbers without SSWs. The lower entries are the corresponding ratios for segregating UTR mutations. The estimates were obtained from the means over genes at the ends of the simulations.

Table S4 The effect of BGS on the numbers of fixations of selectively favorable mutations

Autosomal mutations

Gene No.	Xover Rate	No BGS	With BGS	Ratio (B_2)	B_1
70	0	1.23 (1.17,1.27) 1.58 (1.53,1.62)	0.32 (0.30,0.35) 0.45 (0.42,0.48)	0.263±0.012 0.285±0.017	0.086
	0.5	1.83 (1.77,1.89) 2.94 (2.87,3.02)	1.38 (1.34,1.43) 2.14 (2.08,2.20)	0.754±0.018 0.726±0.014	0.686
	1.0	1.97 (1.87,2.08) 3.10 (2.95,3.26)	1.57 (1.46,1.70) 2.28 (2.13,2.45)	0.797±0.019 0.735±0.021	0.782
	1.5	1.96 (1.88,2.04) 2.94 (2.84,2.99)	1.63 (1.52,1.74) 2.47 (2.26,2.47)	0.831±0.023 0.838±0.021	0.816
	2.0	1.88 (1.82,1.94) 2.92 (2.80,3.04)	1.59 (1.53,1.65) 2.49 (2.37,2.57)	0.844±0.021 0.820±0.018	0.820
	2.5	1.89 (1.83,1.96) 3.04 (2.97,3.11)	1.60 (1.53,1.67) 2.44 (2.37,2.52)	0.845±0.024 0.803±0.015	0.838
140	0	0.90 (0.88,0.93) 1.16 (1.12,1.19)	0.10 (0.09,0.11) 0.13 (0.12,0.14)	0.111±0.006 0.112±0.004	0.043
	0.5	1.87 (1.83,1.92) 2.88 (2.82, 2.99)	1.24 (1.20,1.28) 2.49 (2.42,2.56)	0.659±0.013 0.865±0.017	0.594
	1.0	1.97 (1.90,2.03) 2.95 (2.86,3.05)	1.41 (1.35,1.47) 2.10 (2.02,2.16)	0.717±0.020 0.712±0.017	0.687
	1.5	1.91 (1.85,1.96) 3.01 (2.92,3.09)	1.39 (1.32,1.47) 2.22 (2.15,2.30)	0.728±0.023 0.734±0.017	0.719
	2.0	1.88 (1.84,1.92) 2.95 (2.90,3.00)	1.42 (1.37,1.46) 2.20 (2.15,2.26)	0.752±0.015 0.746±0.012	0.725
	2.5	1.96 (1.92,2.01) 2.98 (2.92,3.05)	1.42 (1.37,1.47) 2.15 (2.10,2.21)	0.723±0.015 0.722±0.012	0.736
210	0	0.75 (0.73,0.77) 0.95 (0.92,0.97)	0.05 (0.04,0.06) 0.07 (0.06,0.08)	0.072±0.007 0.076±0.005	0.029
	0.5	1.86 (1.81,1.90) 2.86 (2.80,2.91)	1.09 (1.06,1.13) 1.66 (1.62,1.70)	0.587±0.012 0.591±0.009	0.525
	1.0	1.87 (1.84,1.91) 2.90 (2.84,2.97)	1.18 (1.10,1.25) 1.85 (1.80,1.91)	0.631±0.021 0.638±0.012	0.605
	1.5	1.85 (1.80,1.90) 2.91 (2.86,2.98)	1.22 (1.17,1.26) 1.89 (2.86,2.98)	0.659±0.015 0.679±0.011	0.640
	2.0	1.89 (1.84,1.93) 2.98 (2.93,3.03)	1.27 (1.25,1.30) 1.95 (1.92,1.99)	0.676±0.008 0.655±0.008	0.639
	2.5	1.92 (1.88,1.96) 2.94 (2.89,2.99)	1.26 (1.23,1.29) 2.01 (1.97,2.05)	0.655±0.010 0.684±0.009	0.657

X- linked mutations with low *s*

Gene No.	Xover Rate	No BGS	With BGS	Ratio (B_2)	B_1
70	0	1.34 (1.29,1.38) 1.83 (1.79,1.86)	0.62 (0.58,0.66) 0.86 (0.83,0.90)	0.461±0.017 0.473±0.011	0.111
	0.5	2.04 (1.97,2.12) 3.24 (3.16,3.33)	1.69 (1.64,1.76) 2.67 (2.61,2.74)	0.832±0.022 0.824±0.015	0.756
	1.0	2.12 (2.08,2.17) 3.31 (3.20,3.43)	1.82 (1.75,1.90) 2.89 (2.82,2.95)	0.858±0.020 0.872±0.018	0.830
	1.5	2.13 (2.06,2.21) 3.31 (3.22,3.41)	1.93 (1.87,1.98) 2.89 (2.81,2.96)	0.904±0.021 0.871±0.017	0.850
	2.0	2.14 (2.04,2.23) 3.34 (3.26,3.40)	1.86 (1.81,1.91) 3.03 (2.96,3.12)	0.871±0.023 0.912±0.016	0.884
	2.5	2.16 (2.03, 2.29) 3.40 (3.31,3.49)	1.93 (1.80, 2.07) 3.02 (2.93,3.10)	0.895±0.042 0.889±0.017	0.878
140	0	1.04 (1.02,1.07) 1.31 (1.28,1.34)	0.27 (0.25,0.29) 0.35 (0.34,0.37)	0.269±0.011 0.269±0.007`	0.054
	0.5	2.08 (2.03,2.14) 3.21 (3.16,3.26)	1.51 (1.48,1.54) 2.10 (2.32,2.41)	0.725±0.012 0.735±0.009	0.682
	1.0	2.10 (2.05,2.15) 3.33 (3.25,3.40)	1.73 (1.69,1.77) 2.60 (2.54,2.67)	0.823±0.014 0.781±0.014	0.785
	1.5	2.07 (2.06,2.17) 3.30 (3.25,3.35)	1.67(1.62,1.72) 2.63 (2.58,2.67)	0.792±0.016 0.796±0.009	0.782
	2.0	2.17 (2.10,2.25) 3.29 (3.24,3.34)	1.73 (1.67,1.78) 2.73 (2.68,2.77)	0.794±0.019 0.830±0.009	0.802
	2.5	2.16 (2.09,2.23) 3.42(3.32,3.51)	1.77 (1.72,1.82) 2.70 (2.64,2.76)	0.820±0.018 0.788±0.014	0.805
210	0	0.85 (0.83,0.87) 1.05 (1.02,1.07)	0.14 (0.13,0.15) 0.16 (0.15,0.18)	0.160±0.003 0.155±0.008	0.042
	0.5	2.02 (1.98,2.05) 3.22 (3.16,3.27)	1.40 (1.36,1.43) 2.16 (2.11,2.21)	0.692±0.011 0.670±0.010	0.623
	1.0	2.13 (2.09,2.17) 3.28 (3.22,3.33)	1.58 (1.54,1.61) 2.42 (2.38,2.45)	0.739±0.010 0.737±0.009	0.714
	1.5	2.12 (2.08,2.16) 3.22 (3.19,3.26)	1.55 (1.50,1.59) 2.42 (2.39,2.46)	0.731±0.013 0.751±0.007	0.720
	2.0	2.12 (2.08,2.16) 3.33 (3.26,3.41)	1.61 (1.57,1.65) 2.48 (2.45,2.51)	0.761±0.012 0.744±0.010	0.747
	2.5	2.13 (2.07,2.18) 3.25 (3.17,3.34)	1.59 (1.53,1.65) 2.44 (2.37,2.50)	0.745±0.017 0.749±0.014	0.739

X- linked mutations: with high *s* and 70 genes

Xover Rate	No BGS	With BGS	Ratio (B_2)	B_1
0	1.72 (1.65,1.80) 2.23 (2.17,2.30)	0.95 (0.91, 0.99) 1.24 (1.19,1.29)	0.548±0.018 0.557±0.014	0.111
0.5	2.69 (2.63,2.75) 4.27 (4.16,4.37)	2.25 (2.18,2.31) 3.42 (3.34,3.50)	0.837±0.016 0.800±0.013	0.756
1.0	2.67 (2.58,2.75) 4.35 (4.22,4.48)	2.37 (2.27,2.46) 3.76 (3.70,3.82)	0.888±0.023 0.864±0.015	0.830
1.5	2.84 (2.72,2.94) 4.49 (4.35,4.61)	2.47 (2.40,2.55) 3.82 (3.73,3.91)	0.872±0.021 0.851±0.016	0.850
2.0	2.81 (2.71,2.90) 4.40 (4.29,4.53)	2.49 (2.40,2.57) 3.91 (3.82,4.01)	0.889±0.022 0.887±0.013	0.884
2.5	2.85 (2.78, 2.92) 4.39 (4.31, 4.48)	2.51 (2.45, 2.57) 3.98 (3.88, 4.07)	0.886±0.015 0.905±0.014	0.878

The upper and lower entries in the cells in the 2nd and 3rd columns show the ratios of the mean numbers of fixations (over the final 20,000 generations) to the number of simulated genes, for selectively favorable NS and UTR mutations, respectively. The 4th column shows the ratios of these values for simulations with and without BGS, respectively, with approximate standard errors calculated from the upper and lower 2.5 percentiles of the numerator and denominator.

The B_1 values in the last column were obtained from the simulation results.

The standard gene conversion parameters are assumed.

Table S5 Analyses of the dispersion of the distribution of numbers of substitutions

Xover rate	**0.5**	**1.0**	**1.5**	**2.0**	**2.5**	**Pooled**
Autosome						
χ^2; d.f.	440; 456	236; 216	316; 336	422; 456	391; 456	1806;1920
χ^2;d.f.	0.965	1.094	0.941	0.925	0.858	0.940
z	– 0.513	0.929	– 0.761	– 1.14	– 2.22	– 1.87
X; low *s*						
χ^2; d.f.	405; 456	272; 336	407; 456	397; 456	383; 395	1864;2099
χ^2;d.f.	0.888	0.818	0.893	0.872	0.969	0.873
z	– 1.73	– 2.58	– 1.65	– 2.00	– 0.434	–3.72
X; high *s*						
χ^2; d.f.	293; 304	270;304	149; 152	152; 152	104; 152	969; 1064
χ^2;d.f.	0.964	0.888	0.983	1.01	0.681	0.911
z	– 0.433	– 1.41	– 0.136	0.0710	– 3.03	– 2.10
Pooled						
χ^2; d.f.	1138;1216	778; 856	873; 944	972; 1064	877; 1003	4639; 5083
χ^2;d.f.	0.936	0.909	0.825	0.914	0.875	0.913
z	– 2.11	– 2.42	– 2.17	– 2.53	– 2.89	– 4.50

The entries in the table were obtained by summing individual χ^2 values and d.f. for the variance to mean ratios for simulations with 70, 140 and 210 genes, for each parameter set, including simulations with and without BGS and using data on both NS and UTR sites. The *z* statistic is Fisher's normal deviate transformation of χ^2, $\sqrt{(2\chi^2)} - \sqrt{2}(\text{d.f.}-0.5)$.

Table S6 Observed and predicted values of neutral diversity (π/θ)for a 70 gene region, relative to the values without hitchhiking effects

Autosomes

Xover Rate	Observed	Integral, NC	Sum., NC	Integral, C	Sum., C
No g.c.					
0.5	0.516 (0.500,0.528) 0.430 (0.419,0.441)	0.582 0.487 0.461	0.612 0.530 0.479	0.471 0.450 0.409	0.507 0.469 0.432
1.0	0.655 (0.637,0.671) 0.555 (0.536,0.573)	0.713 0.597 0.592	0.733 0.610 0.606	0.633 0.545 0.534	0.659 0.562 0.553
1.5	0.735 (0.727,0.743) 0.631 (0.621,0.643)	0.786 0.669 0.664	0.801 0.680 0.676	0.726 0.620 0.621	0.745 0.633 0.635
2.0	0.772 (0.763,0.781) 0.675 (0.666,0.683)	0.832 0.716 0.712	0.843 0.724 0.721	0.784 0.676 0.676	0.799 0.687 0.688
2.5	0.820 (0.812,0.828) 0.715 (0.706,0.724)	0.862 0.744 0.740	0.871 0.750 0.748	0.823 0.711 0.711	0.835 0.720 0.720
G.c.					
0.5	0.685 (0.674,0.695) 0.544 (0.534,0.552)	0.753 0.585 0.578	0.740 0.582 0.575	0.684 0.554 0.539	0.668 0.550 0.535
1.0	0.767 (0.763,0.771) 0.648 (0.626,0.660)	0.821 0.684 0.682	0.813 0.681 0.679	0.771 0.643 0.643	0.761 0.638 0.639
1.5	0.815 (0.809,0.821) 0.703 (0.690,0.717)	0.858 0.731 0.729	0.855 0.729 0.728	0.818 0.697 0.697	0.814 0.695 0.696
2.0	0.850 (0.834,0.856) 0.724 (0.713,0.736)	0.882 0.749 0.748	0.881 0.749 0.748	0.849 0.721 0.721	0.847 0.721 0.721
2.5	0.863 (0.858,0.869) 0.753 (0.744,0.761)	0.899 0.774 0.773	0.899 0.774 0.773	0.871 0.750 0.750	0.871 0.750 0.751

X chromosome

Xover Rate	Observed	Integral, NC	Sum., NC	Integral, C	Sum., C
Small *s*					
0.5	0.570 (0.562,0.580) 0.498 (0.488,0.508)	0.648 0.567 0.547	0.647 0.570 0.550	0.562 0.493 0.498	0.560 0.497 0.502
1.0	0.685 (0.674,0.694) 0.635 (0.626,0.645)	0.734 0.657 0.647	0.732 0.658 0.648	0.668 0.598 0.599	0.665 0.599 0.600
1.5	0.742 (0.733,0.750) 0.673 (0.663,0.683)	0.785 0.704 0.655	0.785 0.706 0.697	0.732 0.657 0.657	0.732 0.658 0.659
2.0	0.781 (0.773,0.789) 0.723 (0.713,0.734)	0.820 0.749 0.741	0.821 0.751 0.743	0.775 0.708 0.708	0.776 0.710 0.711
2.5	0.797 (0.792,0.804) 0.744 (0.732,0.758)	0.845 0.762 0.768	0.847 0.765 0.770	0.806 0.733 0.733	0.809 0.736 0.736
Large *s*					
0.5	0.443 (0.431,0.456) 0.413 (0.405,0.421)	0.525 0.487 0.474	0.532 0.495 0.483	0.434 0.405 0.411	0.443 0.416 0.422
1.0	0.568 (0.558,0.578) 0.528 (0.518,0.539)	0.617 0.572 0.570	0.623 0.579 0.577	0.542 0.499 0.504	0.549 0.508 0.513
1.5	0.631 (0.620,0.642) 0.585 (0.573,0.598)	0.680 0.626 0.625	0.686 0.632 0.631	0.617 0.566 0.570	0.624 0.574 0.577
2.0	0.685 (0.673,0.697) 0.625 (0.611,0.639)	0.725 0.674 0.673	0.732 0.681 0.680	0.671 0.622 0.626	0.679 0.630 0.633
2.5	0.717 (0.708,0.726) 0.672 (0.663,0.681)	0.760 0.701 0.700	0.766 0.708 0.707	0.712 0.656 0.659	0.720 0.664 0.666

The entries for the observed values are the mean synonymous site diversities from the simulations with 70 genes, relative to the corresponding values in the absence of selection at linked sites. The upper and lower entries in each cell are the values with SSWs alone and with SSWs and BGS, respectively.

The upper entries in each cell for the predictions are the reductions with SSWs alone; the middle entries use only the BGS effects estimated from neutral sites (B_1); the lowest entries also include the BGS effects on adaptive substitution rates obtained from the simulations (B_2).

The columns labelled ‘Integral’ use the approximate integral formulae for SSW effects (Equations S24-33); those labelled ‘Sum.’ use the summation formulae, Equations 5 and 6. ‘NC’ denotes predictions without correcting for sweep duration (Equation 5). ‘C’ denotes predictions that correct for sweep duration (Equations 12).
For the summation predictions, corrections for multiple recombination events during the sweep (Equation S20) and for the variance in sweep time (File S1, section 3) were applied.

Table S7 Predicted values of autosomal relative neutral diversity for a 70 gene autosomal region using the summation formula with no correction for interference.

Xover Rate	All three corrections	Sweep duration correction only	Sweep duration + multiple rec. corr.	Sweep duration + sweep coal. time corr.
No g.c.				
0.5	0.494, 0.457	0.475, 0.451	0.468, 0.447	0.501, 0.461
1.0	0.648, 0.549	0.641, 0.547	0.630, 0.539	0.659, 0.556
1.5	0.736, 0.628	0.733, 0.627	0.722, 0.620	0.746, 0,635
2.0	0.791, 0.682	0.790, 0.682	0.780, 0.675	0.800, 0.689
2.5	0.828, 0.715	0.828, 0.716	0.819, 0.709	0.836, 0.721
G.c.				
0.5	0.657, 0.541	0.653, 0.540	0.640, 0.532	0.670, 0.547
1.0	0.752, 0.633	0.752, 0.634	0.739, 0.625	0.764, 0.641
1.5	0.806, 0.690	0.807, 0.692	0.796, 0.684	0.817, 0.698
2.0	0.841, 0.717	0.842, 0.718	0.833, 0.711	0.850, 0.723
2.5	0.865, 0.747	0.866, 0.748	0.858, 0.742	0.873, 0.754

The first entries in each cell are for the case of no BGS; the second entries are for BGS, using the simulation estimate of B_1 for all relevant parameters.

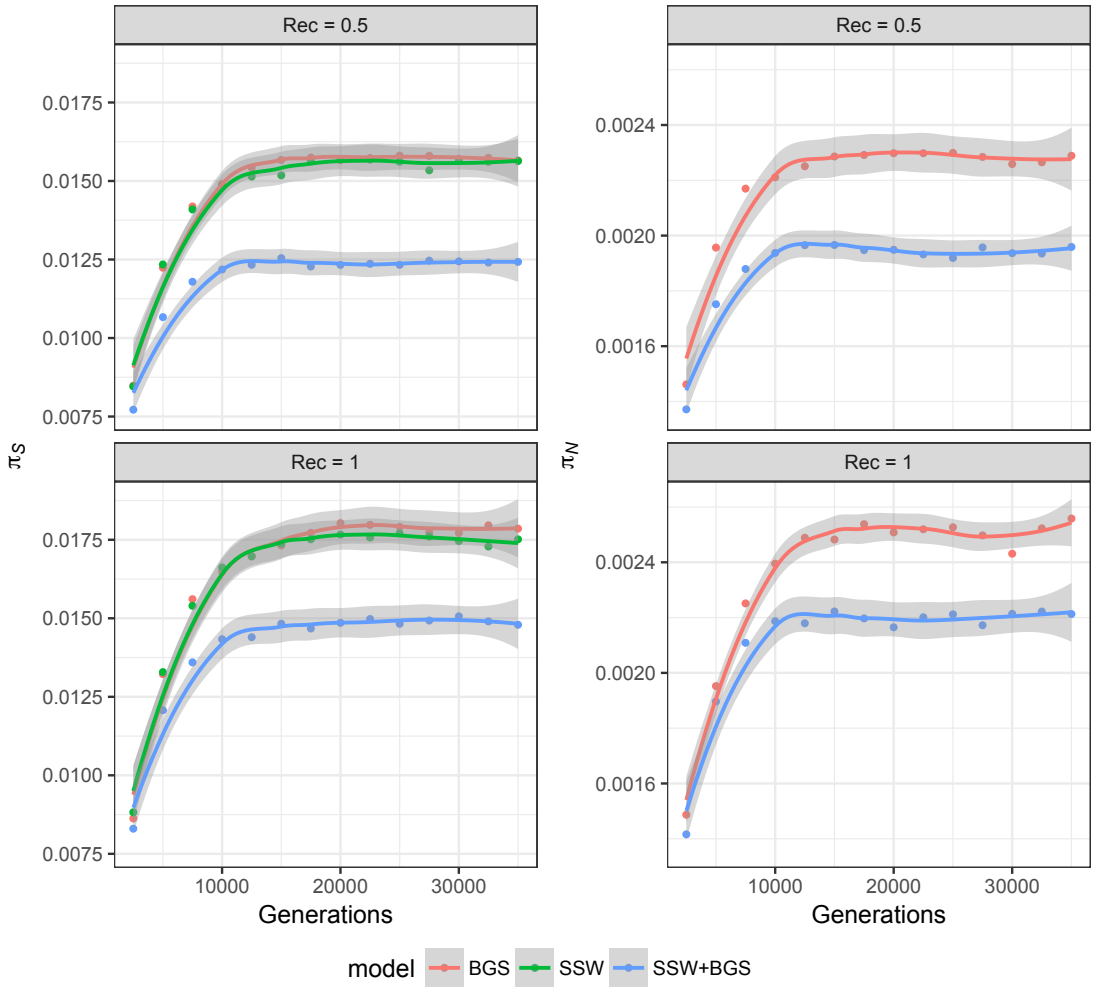

Figure S1. Trajectories of mean synonymous site diversity (π_S) and mean nonsynymous site diversity (π_N) in simulations with the standard rate of crossing over (rec = 1) and with one-half the standard rate (rec = 0.5). Results are shown with BGS alone (BGS), selective sweeps alone (SSW) and with both (SSW+BGS).